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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=1; hr=15; min=18; sec=40; ms=565;]

=====

Reviewer Comments:

<210> 40

<211> 374

<212> PRT

<213> *Pichia pastoris*

<220>

<221> MOD_RES

<222> (176)...(190)

<223> Variable amino acid

<220>

<221> MOD_RES

<222> (202)...(213)

<223> Variable amino acid

<400> 40

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Thr | Asp | Ile | Asp | Phe | Ser | Ser | Tyr | Met | Gln | Gln | Ile | Phe | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Arg | Gln | Gly | Glu | Leu | Asp | Tyr | Ser | Asn | Ile | Phe | Gly | Asp | Thr | Gly |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Pro | Leu | Val | Tyr | Pro | Ala | Gly | His | Val | His | Ala | Tyr | Ser | Val | Leu | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Trp | Tyr | Ser | Asp | Gly | Gly | Glu | Asp | Val | Ser | Phe | Val | Gln | Gln | Ala | Phe |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Gly | Trp | Leu | Tyr | Leu | Gly | Cys | Leu | Leu | Leu | Ser | Ile | Ser | Ser | Tyr | Phe |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Phe | Ser | Gly | Leu | Gly | Lys | Ile | Pro | Pro | Val | Tyr | Phe | Val | Leu | Leu | Val |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ala | Ser | Lys | Arg | Leu | His | Ser | Ile | Phe | Val | Leu | Arg | Leu | Phe | Asn | Asp |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Cys | Leu | Thr | Thr | Phe | Leu | Met | Leu | Ala | Thr | Ile | Ile | Ile | Leu | Gln | Gln | |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Ser | Ser | Trp | Arg | Lys | Asp | Gly | Thr | Thr | Ile | Pro | Leu | Ser | Val | Pro | |
| | | | 130 | | | | | 135 | | | | | 140 | | | |
| Asp | Ala | Ala | Asp | Thr | Tyr | Ser | Leu | Ala | Ile | Ser | Val | Lys | Met | Asn | Xaa | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Cys | Asp | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Glu | Asn | Leu | Ile | Lys | Ala | Leu | Ala | Pro | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | |
| | | | 180 | | | | | 185 | | | | | | 190 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Tyr | Ser | Phe | Ile | Leu | Pro | Leu | His | Tyr | Asp | Asp | |
| | | | 195 | | | | 200 | | | | | | 205 | | | |
| Gln | Ala | Asn | Glu | Ile | Arg | Ser | Ala | Tyr | Phe | Arg | Gln | Ala | Phe | Asp | Phe | |
| | | | 210 | | | | 215 | | | | | 220 | | | | |
| Ser | Arg | Gln | Phe | Leu | Tyr | Lys | Trp | Thr | Val | Asn | Trp | Arg | Phe | Leu | Ser | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Gln | Glu | Thr | Phe | Asn | Asn | Val | His | Phe | His | Gln | Leu | Leu | Phe | Ala | Leu | |
| | | | 245 | | | | | 250 | | | | | | 255 | | |
| His | Ile | Ile | Thr | Leu | Val | Leu | Phe | Ile | Leu | Lys | Phe | Leu | Ser | Pro | Lys | |
| | | | 260 | | | | | 265 | | | | | | 270 | | |
| Asn | Ile | Gly | Lys | Pro | Leu | Gly | Arg | Phe | Val | Leu | Asp | Ile | Phe | Lys | Phe | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Trp | Lys | Pro | Thr | Leu | Ser | Pro | Thr | Asn | Ile | Ile | Asn | Asp | Pro | Glu | Arg | |
| | | 290 | | | | 295 | | | | | | 300 | | | | |
| Ser | Pro | Asp | Phe | Val | Tyr | Thr | Val | Met | Ala | Thr | Thr | Asn | Leu | Ile | Gly | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Val | Leu | Phe | Ala | Arg | Ser | Leu | His | Tyr | Gln | Phe | Leu | Ser | Trp | Tyr | Ala | |
| | | | 325 | | | | | 330 | | | | | | 335 | | |
| Phe | Ser | Leu | Pro | Tyr | Leu | Leu | Tyr | Lys | Ala | Arg | Leu | Asn | Phe | Ile | Ala | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Ser | Ile | Ile | Val | Tyr | Ala | Ala | His | Glu | Tyr | Cys | Trp | Leu | Val | Phe | Pro | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Ala | Thr | Glu | Gln | Ser | Ser | | | | | | | | | | | |
| | | | 370 | | | | | | | | | | | | | |

The above <222> responses describing Xaa locations are incorrect: Xaa is located at positions 160-174 and 186-197, not at locations 202-213.

Application No: 10500240 Version No: 3.0

Input Set:**Output Set:**

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (17) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (18) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (19) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (20) |

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

| Error code | Error Description |
|------------|---|
| | This error has occurred more than 20 times, will not be displayed |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (24) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (24) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (26) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (36) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (36) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (38) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (38) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (40) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (40) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (160) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (161) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (162) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (163) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (164) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (165) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (166) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (167) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (168) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (169) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (170) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (171) |

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

| Error code | Error Description |
|------------|--|
| E 341 | 'Xaa' position not defined SEQID (40) POS (172) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (173) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (174) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (191) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (192) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (193) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (194) |
| E 341 | 'Xaa' position not defined SEQID (40) POS (195) This error has occurred more than 20 times, will not be displayed |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (42) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (42) |
| W 402 | Undefined organism found in <213> in SEQ ID (44) |
| W 402 | Undefined organism found in <213> in SEQ ID (45) |
| W 402 | Undefined organism found in <213> in SEQ ID (46) |
| W 402 | Undefined organism found in <213> in SEQ ID (48) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (54) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (56) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (58) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (60) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (62) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (68) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (70) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (72) |

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

| Error code | Error Description |
|------------|--|
| E 257 | Invalid sequence data feature in <221> in SEQ ID (78) This error has occurred more than 20 times, will not be displayed |
| W 402 | Undefined organism found in <213> in SEQ ID (86) |
| W 402 | Undefined organism found in <213> in SEQ ID (87) |
| W 402 | Undefined organism found in <213> in SEQ ID (88) |
| W 402 | Undefined organism found in <213> in SEQ ID (90) |
| W 402 | Undefined organism found in <213> in SEQ ID (92) |
| W 402 | Undefined organism found in <213> in SEQ ID (94) |

SEQUENCE LISTING

<110> WILDT, Stefan
MIELE, Robert G.
NETT, Juergen H.
DAVIDSON, Robert C.

<120> METHODS TO ENGINEER MAMMALIAN-TYPE
CARBOHYDRATE STRUCTURES

<130> GF0022P

<140> 10500240
<141> 2005-03-23

<150> PCT/US02/41510
<151> 2002-12-24

<150> 60/344,169
<151> 2001-12-27

<160> 106

<170> FastSEQ for Windows Version 4.0

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gggtgttttgt tttctagatc tttgcaytay cartt 35

<210> 2
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 2
agaatttggt gggtgaagaat tccarcacca ytcrtg 36

<210> 3
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

| | |
|-------------------------------------|----|
| <400> 3 | |
| cctaagctgg tatgcgttct ctttgccata tc | 32 |
| <210> 4 | |
| <211> 30 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 4 | |
| gcggcataaaa caataataga tgctataaag | 30 |
| <210> 5 | |
| <211> 20 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 5 | |
| aattaaccct cactaaaggg | 20 |
| <210> 6 | |
| <211> 22 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 6 | |
| gtaatacgac tcactatagg gc | 22 |
| <210> 7 | |
| <211> 24 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 7 | |
| ccacatcatc cgtgctacat atag | 24 |
| <210> 8 | |
| <211> 44 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 8 | |

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<210> 9

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<213> Artificial Sequence

<220>

<223> Primer

<400> 9

ccatccagtgc tcgaaaacga gccaatgggt catgtctata aatc 44

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 10

agcctcagcg ccaacaagcg atgg 24

<210> 11

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ctggataacc ctcgatactt cgagatctgt ttagcttgcc tcgt 44

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

gatttataga catgaaccat tggctcggtt tcgacactgg atgg 44

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 13

atcctttacc gatgctgtat 20

| | |
|--|----|
| <210> 14 | |
| <211> 27 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 14 | |
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| <210> 15 | |
| <211> 36 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 15 | |
| tcctggcgcg ccttcccgag agaactggcc tccttc | 36 |
| <210> 16 | |
| <211> 37 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 16 | |
| aattaattaa ccctagccct ccgctgtatc caacttg | 37 |
| <210> 17 | |
| <211> 28 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 17 | |
| aatgagatga ggctccgcaa tggaactg | 28 |
| <210> 18 | |
| <211> 28 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
| <223> Primer | |
| <400> 18 | |
| ctgattgctt atcaacgaga attccttg | 28 |
| <210> 19 | |
| <211> 28 | |

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 19
 tgtttggtttc tcagatgatc agttggtg 28

 <210> 20
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 20
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 <210> 21
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 21
 aatcaagtg gatgaaggac atgtggc 27

 <210> 22
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 22
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 <210> 23
 <211> 4
 <212> PRT
 <213> Saccharomyces cerevisiae

 <400> 23
 His Asp Glu Leu
 1

 <210> 24
 <211> 458
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 <213> Saccharomyces cerevisiae

<220>
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<222> (304)...(318)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (416)...(436)
<223> Variable amino acid

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1 5 10 15
Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
20 25 30
Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
35 40 45
Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
50 55 60
Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
65 70 75 80
Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
85 90 95
Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
100 105 110
Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
115 120 125
Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
130 135 140
Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145 150 155 160
Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
165 170 175
Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
180 185 190
Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
195 200 205
Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
210 215 220
Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225 230 235 240
Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
245 250 255
Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
260 265 270
His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
275 280 285
Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
290 295 300
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
305 310 315 320
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
325 330 335
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
340 345 350
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
355 360 365

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | His | Tyr | Gln | Phe | Leu | Ser | Trp | Tyr | His | Trp | Thr | Leu | Pro | Ile |
| 370 | | | | | | 375 | | | | | 380 | | | | |
| Leu | Ile | Phe | Trp | Ser | Gly | Met | Pro | Phe | Phe | Val | Gly | Pro | Ile | Trp | Tyr |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Val | Leu | His | Glu | Trp | Cys | Trp | Asn | Ser | Tyr | Pro | Pro | Asn | Ser | Gln | Xaa |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 420 | | | | | 425 | | | | | | 430 | |
| Xaa | Xaa | Xaa | Xaa | Ser | Gly | Ser | Val | Ala | Leu | Ala | Lys | Ser | His | Leu | Arg |
| | | | 435 | | | | 440 | | | | | | 445 | | |
| Thr | Thr | Ser | Ser | Met | Glu | Lys | Lys | Leu | Asn | | | | | | |
| | | | 450 | | | | 455 | | | | | | | | |

<210> 25

<211> 458

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 25

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Glu | Gln | Ser | Pro | Gln | Gly | Glu | Lys | Ser | Leu | Gln | Arg | Lys |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Gln | Phe | Val | Arg | Pro | Pro | Leu | Asp | Leu | Trp | Gln | Asp | Leu | Lys | Asp | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Arg | Tyr | Val | Ile | Phe | Asp | Cys | Arg | Ala | Asn | Leu | Ile | Val | Met | Pro |
| | | | 35 | | | | 40 | | | | | | 45 | | |
| Leu | Leu | Ile | Leu | Phe | Glu | Ser | Met | Leu | Cys | Lys | Ile | Ile | Ile | Lys | Lys |
| | | | 50 | | | | 55 | | | | | | 60 | | |
| Val | Ala | Tyr | Thr | Glu | Ile | Asp | Tyr | Lys | Ala | Tyr | Met | Glu | Gln | Ile | Glu |
| | | | | | 70 | | | | | 75 | | | | | 80 |
| Met | Ile | Gln | Leu | Asp | Gly | Met | Leu | Asp | Tyr | Ser | Gln | Val | Ser | Gly | Gly |
| | | | | | 85 | | | | 90 | | | | | 95 | |
| Thr | Gly | Pro | Leu | Val | Tyr | Pro | Ala | Gly | His | Val | Leu | Ile | Tyr | Lys | Met |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Met | Tyr | Trp | Leu | Thr | Glu | Gly | Met | Asp | His | Val | Glu | Arg | Gly | Gln | Val |
| | | | 115 | | | | 120 | | | | | | 125 | | |
| Phe | Phe | Arg | Tyr | Leu | Tyr | Leu | Leu | Thr | Leu | Ala | Leu | Gln | Met | Ala | Cys |
| | | | 130 | | | | 135 | | | | | 140 | | | |
| Tyr | Tyr | Leu | Leu | His | Leu | Pro | Pro | Trp | Cys | Val | Val | Leu | Ala | Cys | Leu |
| | | | | | 150 | | | | | 155 | | | | | 160 |
| Ser | Lys | Arg | Leu | His | Ser | Ile | Tyr | Val | Leu | Arg | Leu | Phe | Asn | Asp | Cys |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Phe | Thr | Thr | Leu | Phe | Met | Val | Val | Thr | Val | Leu | Gly | Ala | Ile | Val | Ala |
| | | | 180 | | | | | 185 | | | | | | 190 | |
| Ser | Arg | Cys | His | Gln | Arg | Pro | Lys | Leu | Lys | Lys | Ser | Leu | Ala | Leu | Val |
| | | | 195 | | | | 200 | | | | | | 205 | | |
| Ile | Ser | Ala | Thr | Tyr | Ser | Met | Ala | Val | Ser | Ile | Lys | Met | Asn | Ala | Leu |
| | | | 210 | | | | 215 | | | | | 220 | | | |
| Leu | Tyr | Phe | Pro | Ala | Met | Met | Ile | Ser | Leu | Phe | Ile | Leu | Asn | Asp | Ala |
| | | | | | 230 | | | | | 235 | | | | | 240 |
| Asn | Val | Ile | Leu | Thr | Leu | Leu | Asp | Leu | Val | Ala | Met | Ile | Ala | Trp | Gln |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Val | Ala | Val | Ala | Val | Pro | Phe | Leu | Arg | Ser | Phe | Pro | Gln | Gln | Tyr | Leu |
| | | | 260 | | | | | 265 | | | | | | 270 | |
| His | Cys | Ala | Phe | Asn | Phe | Gly | Arg | Lys | Phe | Met | Tyr | Gln | Trp | Ser | Ile |
| | | | 275 | | | | 280 | | | | | | 285 | | |
| Asn | Trp | Gln | Met | Met | Asp | Glu | Glu | Ala | Phe | Asn | Asp | Lys | Arg | Phe | His |

290 295 300
 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
 305 310 315 320
 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 325 330 335
 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
 340 345 350
 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
 355 360 365
 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
 370 375 380
 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385 390 395 400
 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
 405 410 415
 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
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<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

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<222> (333)...(347)

<223> Variable amino acid

<400> 26

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 Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
 35 40 45
 Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
 50 55 60
 Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
 65 70 75 80
 His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
 85 90 95
 His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr
 100 105 110
 Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp
 115 120 125
 Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val
 130 135 140
 Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr
 145 150 155 160
 Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu
 165 170 175
 Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met

[illegible]